

SEQUENCE LISTING

<110> Ruan, Yong-Ling
Furbank, Robert T.
Danny, Llewellyn J.

<120> Modification of sucrose synthase gene expression in plant tissue and uses therefor

<130> GHSUSY WO1

<150> 60/251852

<151> 2000-12-08

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 2625

<212> DNA

<213> Gossypium hirsutum

<220>

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<223> n = any nucleotide (a,g,c,t)

<220>

<221> CDS

<222> (1)..(2625)

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Met Ala Glu Arg Ala Leu Thr Arg Val His Ser Leu Arg Glu Arg Leu	
1 5 10 15	

gat gag acc ctt ctt gct cac agg aac gag att ttg gcc ttg ctc tca	96
Asp Glu Thr Leu Leu Ala His Arg Asn Glu Ile Leu Ala Leu Leu Ser	
20 25 30	

agg atc gag ggc aaa gga aaa gga att ctg caa cac cat caa att att	144
Arg Ile Glu Gly Lys Gly Lys Gly Ile Leu Gln His His Gln Ile Ile	
35 40 45	

cta gag ttt gaa gct atc cct gaa gag aac aga aag aag ctc gct aat	192
Leu Glu Phe Glu Ala Ile Pro Glu Glu Asn Arg Lys Lys Leu Ala Asn	
50 55 60	

ggg gca ttt ttt gaa gta ttg aag gct agt cag gaa gcg atc gtg ttg	240
Gly Ala Phe Phe Glu Val Leu Lys Ala Ser Gln Glu Ala Ile Val Leu	
65 70 75 80	

cct cca tgg gtt gca ctt gct gtt cgt cca agg cct ggt gtt tgg gag	288
Pro Pro Trp Val Ala Leu Ala Val Arg Pro Arg Pro Gly Val Trp Glu	

85								90				95					
tac	att	aga	gtg	aat	gtt	cac	gcc	ctt	gtt	gtt	gag	gaa	ctc	act	gtt	336	
Tyr	Ile	Arg	Val	Asn	Val	His	Ala	Leu	Val	Val	Glu	Glu	Leu	Thr	Val		
			100					105					110				
gct	gag	tat	ctc	cac	ttc	aag	gaa	gag	ctt	gtt	gat	gga	agt	tca	aat	384	
Ala	Glu	Tyr	Leu	His	Phe	Lys	Glu	Glu	Leu	Val	Asp	Gly	Ser	Ser	Asn		
		115					120					125					
gga	aac	ttt	gtt	ttg	gaa	ttg	gat	ttt	gag	ccc	ttc	aac	tca	tca	ttc	432	
Gly	Asn	Phe	Val	Leu	Glu	Leu	Asp	Phe	Glu	Pro	Phe	Asn	Ser	Ser	Phe		
	130					135					140						
ccc	cgc	cca	act	ctt	tca	aaa	tcc	att	ggg	aat	ggg	gtg	gag	ttc	cta	480	
Pro	Arg	Pro	Thr	Leu	Ser	Lys	Ser	Ile	Gly	Asn	Gly	Val	Glu	Phe	Leu		
145					150					155					160		
aat	cgt	cac	ctt	tcg	gca	aaa	ttg	ttc	cat	gac	aag	gag	agc	atg	cac	528	
Asn	Arg	His	Leu	Ser	Ala	Lys	Leu	Phe	His	Asp	Lys	Glu	Ser	Met	His		
			165					170						175			
cct	ttg	ctc	gaa	ttc	ctc	aga	gtc	cat	tgt	cac	aag	ggc	aag	aac	atg	576	
Pro	Leu	Leu	Glu	Phe	Leu	Arg	Val	His	Cys	His	Lys	Gly	Lys	Asn	Met		
			180					185					190				
atg	ttg	aat	gac	aga	att	cag	aac	ttg	aat	gct	ctt	caa	cat	gtt	ttg	624	
Met	Leu	Asn	Asp	Arg	Ile	Gln	Asn	Leu	Asn	Ala	Leu	Gln	His	Val	Leu		
		195					200					205					
agg	aaa	gca	gag	gag	tat	ctt	ggg	acc	cta	cct	cct	gag	aca	cca	tgt	672	
Arg	Lys	Ala	Glu	Glu	Tyr	Leu	Gly	Thr	Leu	Pro	Pro	Glu	Thr	Pro	Cys		
	210					215					220						
gcc	gaa	ttc	gaa	cac	cgg	ttc	cag	gaa	atc	ggg	ttg	gaa	aga	ggg	tgg	720	
Ala	Glu	Phe	Glu	His	Arg	Phe	Gln	Glu	Ile	Gly	Leu	Glu	Arg	Gly	Trp		
225					230				235						240		
ggg	gac	acc	gca	gaa	cgc	gtg	ctc	gag	atg	atc	caa	ctc	ctt	ttg	gat	768	
Gly	Asp	Thr	Ala	Glu	Arg	Val	Leu	Glu	Met	Ile	Gln	Leu	Leu	Leu	Asp		
			245						250					255			
ctt	ctt	gag	gca	act	gat	cct	tgc	acc	ctt	gag	aag	ttc	ctt	ggg	aga	816	
Leu	Leu	Glu	Ala	Thr	Asp	Pro	Cys	Thr	Leu	Glu	Lys	Phe	Leu	Gly	Arg		
			260					265					270				
atc	ccc	atg	gtg	ttc	aat	gtt	gtg	att	ctc	act	ccc	cac	gga	tac	ttc	864	
Ile	Pro	Met	Val	Phe	Asn	Val	Val	Ile	Leu	Thr	Pro	His	Gly	Tyr	Phe		
		275					280					285					
gct	caa	gac	aat	gtt	ttg	ggg	tat	ccc	gac	acc	ggg	ggg	cag	gtt	gtt	912	
Ala	Gln	Asp	Asn	Val	Leu	Gly	Tyr	Pro	Asp	Thr	Gly	Gly	Gln	Val	Val		
	290					295					300						
tac	atc	ttg	gat	caa	gtc	cga	gct	ttg	gag	aat	gag	atg	ctc	ctc	cgt	960	
Tyr	Ile	Leu	Asp	Gln	Val	Arg	Ala	Leu	Glu	Asn	Glu	Met	Leu	Leu	Arg		
305					310					315					320		

ata aag caa caa gga ctc aac atc acc cct cga atc ctc att att act	1008
Ile Lys Gln Gln Gly Leu Asn Ile Thr Pro Arg Ile Leu Ile Ile Thr	
325 330 335	
aga ctt ctt cct gat gct gtc gga aca aca tgc ggt caa cga ctt gag	1056
Arg Leu Leu Pro Asp Ala Val Gly Thr Thr Cys Gly Gln Arg Leu Glu	
340 345 350	
aaa gta tac gga aca gag cac tcg gat att ctt cga gta ccc ttc aga	1104
Lys Val Tyr Gly Thr Glu His Ser Asp Ile Leu Arg Val Pro Phe Arg	
355 360 365	
aca gaa aag gga att gtt cga aaa tgg atc tca aga ttt gaa aaa gtc	1152
Thr Glu Lys Gly Ile Val Arg Lys Trp Ile Ser Arg Phe Glu Lys Val	
370 375 380	
tgg cca tac ttg gaa acc tac aca gag gat gtt gct cat gaa atc tcc	1200
Trp Pro Tyr Leu Glu Thr Tyr Thr Glu Asp Val Ala His Glu Ile Ser	
385 390 395 400	
aaa gag ttg cac ggc acg cca gat ctg atc atc gga aac nac agc gac	1248
Lys Glu Leu His Gly Thr Pro Asp Leu Ile Ile Gly Asn Xaa Ser Asp	
405 410 415	
ggc aat atc gtc gcc tcc ttg ctc gca cat aaa tta ggt gtc aca cag	1296
Gly Asn Ile Val Ala Ser Leu Leu Ala His Lys Leu Gly Val Thr Gln	
420 425 430	
tgc acc atc gcc cat gct ttg gag aag aca aaa tat cca gat tca gat	1344
Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asp Ser Asp	
435 440 445	
atc tat tgg aag aag ctt gaa gac aaa tac cat ttc tct tgc caa ttt	1392
Ile Tyr Trp Lys Lys Leu Glu Asp Lys Tyr His Phe Ser Cys Gln Phe	
450 455 460	
aca gct gat ctt ttt gca atg aac cat aca gat ttc atc atc acc agt	1440
Thr Ala Asp Leu Phe Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser	
465 470 475 480	
act ttc cag gaa att gca gga agc aag gac act gtt ggt caa tac gag	1488
Thr Phe Gln Glu Ile Ala Gly Ser Lys Asp Thr Val Gly Gln Tyr Glu	
485 490 495	
agc cac act gct ttc act ctt cct ggt ctc tac cgt gtt gta cat ggt	1536
Ser His Thr Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly	
500 505 510	
atc gat gtg ttt gat ccc aaa ttc aac att gtt tcc cct ggt gct gat	1584
Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp	
515 520 525	
atg gag ata tac ttc cct tac acc gaa gag aag cgg agg ttg aag cat	1632
Met Glu Ile Tyr Phe Pro Tyr Thr Glu Glu Lys Arg Arg Leu Lys His	
530 535 540	
ttc cat cct gag atc gaa gac ctt ctt tac acc aaa gtt gag aat gaa	1680
Phe His Pro Glu Ile Glu Asp Leu Leu Tyr Thr Lys Val Glu Asn Glu	

545		550		555		560	
gaa cac tta tgt gtg ctc aat gac cgc aac aag cca att ctg ttc aca							1728
Glu His Leu Cys Val Leu Asn Asp Arg Asn Lys Pro Ile Leu Phe Thr							
		565		570		575	
atg cca agg ctt gat cgt gtc aag aac tta acc gga ctc gtc gag tgg							1776
Met Pro Arg Leu Asp Arg Val Lys Asn Leu Thr Gly Leu Val Glu Trp							
		580		585		590	
tgc ggc aag aac cca aag ttg cgt gag ttg gct aac ctc gta gtt gta							1824
Cys Gly Lys Asn Pro Lys Leu Arg Glu Leu Ala Asn Leu Val Val Val							
		595		600		605	
ggg ggt gat agg cga aag gaa tct aaa gat ttg gaa gag aag gct gaa							1872
Gly Gly Asp Arg Arg Lys Glu Ser Lys Asp Leu Glu Lys Ala Glu							
		610		615		620	
atg aag aaa atg ttt gag ctg atc gac aag tac aac ttg aac ggc caa							1920
Met Lys Lys Met Phe Glu Leu Ile Asp Lys Tyr Asn Leu Asn Gly Gln							
		625		630		635	640
ttc aga tgg ata tca tct caa atg aac aga atc cga aat gtt gaa ctt							1968
Phe Arg Trp Ile Ser Ser Gln Met Asn Arg Ile Arg Asn Val Glu Leu							
		645		650		655	
tac cga tac att tgc gac acg aaa ggt gcc ttt gta cag cct gca ttg							2016
Tyr Arg Tyr Ile Cys Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Leu							
		660		665		670	
tat gaa gcc ttt gga ttg aca gtt gtg gag gca atg act tgc ggt ttg							2064
Tyr Glu Ala Phe Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu							
		675		680		685	
cca aca ttc gca acc tgt aac ggt gga cca gcc gag att att gtc cat							2112
Pro Thr Phe Ala Thr Cys Asn Gly Gly Pro Ala Glu Ile Ile Val His							
		690		695		700	
ggg aaa tct ggt ttc aac att gat cct tac cat ggt gat caa gct gct							2160
Gly Lys Ser Gly Phe Asn Ile Asp Pro Tyr His Gly Asp Gln Ala Ala							
		705		710		715	720
gac ata ctc gtc gat ttc ttt gaa aag tgt aag aaa gat cca tct cac							2208
Asp Ile Leu Val Asp Phe Phe Glu Lys Cys Lys Lys Asp Pro Ser His							
		725		730		735	
tgg gat aag atc tcc caa gga ggc ttg aaa cga ata gag gag aag tat							2256
Trp Asp Lys Ile Ser Gln Gly Gly Leu Lys Arg Ile Glu Glu Lys Tyr							
		740		745		750	
aca tgg aag att tac tcg gag aga cta ttg acc ctg aca gga gtg tat							2304
Thr Trp Lys Ile Tyr Ser Glu Arg Leu Leu Thr Leu Thr Gly Val Tyr							
		755		760		765	
gga ttc tgg aag cat gtt tcc aac ctt gaa cgc cgt gag agt cgt cgt							2352
Gly Phe Trp Lys His Val Ser Asn Leu Glu Arg Arg Glu Ser Arg Arg							
		770		775		780	

tac ctt gag atg ttt tat gct ctt aag tac cgt aag ctg gct gaa tca	2400
Tyr Leu Glu Met Phe Tyr Ala Leu Lys Tyr Arg Lys Leu Ala Glu Ser	
785 790 795 800	
gtt cca ttg gca gag gag taa att gaa cct gtt aaa taa cat tgg gcc	2448
Val Pro Leu Ala Glu Glu Ile Glu Pro Val Lys His Trp Ala	
805 810	
ggg ttt tct tgg aga ata ata ttc tgt ttt gta att tca att gga gaa	2496
Gly Phe Ser Trp Arg Ile Ile Phe Cys Phe Val Ile Ser Ile Gly Glu	
815 820 825 830	
gct cct ttg tat ttc atc ttg tct ttt cct ttt cct ttt ttc gcc ggc	2544
Ala Pro Leu Tyr Phe Ile Leu Ser Phe Pro Phe Pro Phe Phe Ala Gly	
835 840 845	
att gtt tga aca tgg ggt tgt gcg ccc gtc aat tcc agt taa ata tgg	2592
Ile Val Thr Trp Gly Cys Ala Pro Val Asn Ser Ser Ile Trp	
850 855 860	
tga ctt ttg ttt ttc aaa aaa aaa aaa aaa aaa	2625
Leu Leu Phe Phe Lys Lys Lys Lys Lys Lys	
865 870	

<210> 2
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 <212> PRT
 <213> Gossypium hirsutum

<220>
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 <222> (414)..(414)
 <223> The 'Xaa' at location 414 stands for Asn, Asp, His, or Tyr.

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20 25 30

Arg Ile Glu Gly Lys Gly Lys Gly Ile Leu Gln His His Gln Ile Ile
35 40 45

Leu Glu Phe Glu Ala Ile Pro Glu Glu Asn Arg Lys Lys Leu Ala Asn
50 55 60

Gly Ala Phe Phe Glu Val Leu Lys Ala Ser Gln Glu Ala Ile Val Leu
65 70 75 80

Pro Pro Trp Val Ala Leu Ala Val Arg Pro Arg Pro Gly Val Trp Glu
85 90 95

Tyr Ile Arg Val Asn Val His Ala Leu Val Val Glu Glu Leu Thr Val
100 105 110

Ala Glu Tyr Leu His Phe Lys Glu Glu Leu Val Asp Gly Ser Ser Asn
115 120 125

Gly Asn Phe Val Leu Glu Leu Asp Phe Glu Pro Phe Asn Ser Ser Phe
130 135 140

Pro Arg Pro Thr Leu Ser Lys Ser Ile Gly Asn Gly Val Glu Phe Leu
145 150 155 160

Asn Arg His Leu Ser Ala Lys Leu Phe His Asp Lys Glu Ser Met His
165 170 175

Pro Leu Leu Glu Phe Leu Arg Val His Cys His Lys Gly Lys Asn Met
180 185 190

Met Leu Asn Asp Arg Ile Gln Asn Leu Asn Ala Leu Gln His Val Leu
195 200 205

Arg Lys Ala Glu Glu Tyr Leu Gly Thr Leu Pro Pro Glu Thr Pro Cys
210 215 220

Ala Glu Phe Glu His Arg Phe Gln Glu Ile Gly Leu Glu Arg Gly Trp
225 230 235 240

Gly Asp Thr Ala Glu Arg Val Leu Glu Met Ile Gln Leu Leu Leu Asp
245 250 255

Leu Leu Glu Ala Thr Asp Pro Cys Thr Leu Glu Lys Phe Leu Gly Arg
260 265 270

Ile Pro Met Val Phe Asn Val Val Ile Leu Thr Pro His Gly Tyr Phe
275 280 285

Ala Gln Asp Asn Val Leu Gly Tyr Pro Asp Thr Gly Gly Gln Val Val
290 295 300

Tyr Ile Leu Asp Gln Val Arg Ala Leu Glu Asn Glu Met Leu Leu Arg
 305 310 315 320

Ile Lys Gln Gln Gly Leu Asn Ile Thr Pro Arg Ile Leu Ile Ile Thr
 325 330 335

Arg Leu Leu Pro Asp Ala Val Gly Thr Thr Cys Gly Gln Arg Leu Glu
 340 345 350

Lys Val Tyr Gly Thr Glu His Ser Asp Ile Leu Arg Val Pro Phe Arg
 355 360 365

Thr Glu Lys Gly Ile Val Arg Lys Trp Ile Ser Arg Phe Glu Lys Val
 370 375 380

Trp Pro Tyr Leu Glu Thr Tyr Thr Glu Asp Val Ala His Glu Ile Ser
 385 390 395 400

Lys Glu Leu His Gly Thr Pro Asp Leu Ile Ile Gly Asn Xaa Ser Asp
 405 410 415

Gly Asn Ile Val Ala Ser Leu Leu Ala His Lys Leu Gly Val Thr Gln
 420 425 430

Cys Thr Ile Ala His Ala Leu Glu Lys Thr Lys Tyr Pro Asp Ser Asp
 435 440 445

Ile Tyr Trp Lys Lys Leu Glu Asp Lys Tyr His Phe Ser Cys Gln Phe
 450 455 460

Thr Ala Asp Leu Phe Ala Met Asn His Thr Asp Phe Ile Ile Thr Ser
 465 470 475 480

Thr Phe Gln Glu Ile Ala Gly Ser Lys Asp Thr Val Gly Gln Tyr Glu
 485 490 495

Ser His Thr Ala Phe Thr Leu Pro Gly Leu Tyr Arg Val Val His Gly
 500 505 510

Ile Asp Val Phe Asp Pro Lys Phe Asn Ile Val Ser Pro Gly Ala Asp
 515 520 525

Met Glu Ile Tyr Phe Pro Tyr Thr Glu Glu Lys Arg Arg Leu Lys His
 530 535 540

Phe His Pro Glu Ile Glu Asp Leu Leu Tyr Thr Lys Val Glu Asn Glu
 545 550 555 560

Glu His Leu Cys Val Leu Asn Asp Arg Asn Lys Pro Ile Leu Phe Thr
 565 570 575

Met Pro Arg Leu Asp Arg Val Lys Asn Leu Thr Gly Leu Val Glu Trp
 580 585 590

Cys Gly Lys Asn Pro Lys Leu Arg Glu Leu Ala Asn Leu Val Val Val
 595 600 605

Gly Gly Asp Arg Arg Lys Glu Ser Lys Asp Leu Glu Glu Lys Ala Glu
 610 615 620

Met Lys Lys Met Phe Glu Leu Ile Asp Lys Tyr Asn Leu Asn Gly Gln
 625 630 635 640

Phe Arg Trp Ile Ser Ser Gln Met Asn Arg Ile Arg Asn Val Glu Leu
 645 650 655

Tyr Arg Tyr Ile Cys Asp Thr Lys Gly Ala Phe Val Gln Pro Ala Leu
 660 665 670

Tyr Glu Ala Phe Gly Leu Thr Val Val Glu Ala Met Thr Cys Gly Leu
 675 680 685

Pro Thr Phe Ala Thr Cys Asn Gly Gly Pro Ala Glu Ile Ile Val His
 690 695 700

Gly Lys Ser Gly Phe Asn Ile Asp Pro Tyr His Gly Asp Gln Ala Ala
 705 710 715 720

Asp Ile Leu Val Asp Phe Phe Glu Lys Cys Lys Lys Asp Pro Ser His
 725 730 735

Trp Asp Lys Ile Ser Gln Gly Gly Leu Lys Arg Ile Glu Glu Lys Tyr
 740 745 750

Thr Trp Lys Ile Tyr Ser Glu Arg Leu Leu Thr Leu Thr Gly Val Tyr
 755 760 765

Gly Phe Trp Lys His Val Ser Asn Leu Glu Arg Arg Glu Ser Arg Arg
 770 775 780

Tyr Leu Glu Met Phe Tyr Ala Leu Lys Tyr Arg Lys Leu Ala Glu Ser
 785 790 795 800

Val Pro Leu Ala Glu Glu
 805

<210> 3
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 <212> PRT
 <213> Gossypium hirsutum

<220>
 <221> misc_feature
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Ile Glu Pro Val Lys
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<210> 4
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 <213> Gossypium hirsutum

<220>
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 <223> n = any nucleotide (a,g,c,t)

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His Trp Ala Gly Phe Ser Trp Arg Ile Ile Phe Cys Phe Val Ile Ser
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Ile Gly Glu Ala Pro Leu Tyr Phe Ile Leu Ser Phe Pro Phe Pro Phe
 20 25 30

Phe Ala Gly Ile Val
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<210> 5
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 <213> Gossypium hirsutum

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<220>
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<223> n = any nucleotide (a,g,c,t)

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<210> 6
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Leu Leu Phe Phe Lys Lys Lys Lys Lys Lys
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